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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/981,421

DATE: 11/02/2001
TIME: 15:08:38

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Output Set: N:\CRF3\11022001\I981421.raw

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 3 <110> APPLICANT: Sims, John E.
 4         Mohler, Kendall M.
 5         Born, Teresa L.
 7 <120> TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
 9 <130> FILE REFERENCE: 3086-A
C-->11 <140> CURRENT APPLICATION NUMBER: US/09/981,421
12 <141> CURRENT FILING DATE: 2001-10-17
14 <150> PRIOR APPLICATION NUMBER: US 60/241,408
15 <151> PRIOR FILING DATE: 2000-10-18
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2681
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (484)..(2283)
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37 ttatgtctta agagcaggaa ataaagagac agctgaaggt gtagccttga ccaactgaaa     180
39 gggaaatctt catcctctga aaaaacatat gtgattctca aaaaacgcat ctggaaaatt     240
41 gataaagaag cgattctgta gattctccca gcgctgttgg gctctcaatt ccttctgtga     300
43 aggacaacat atggtgatgg ggaaatcaga agctttgaga ccctctacac ctggatatga     360
45 atccccctttc taatacttac cagaaatgaa ggggatactc agggcagagt tctgaatctc     420
47 aaaacactct actctggcaa aggaatgaag ttattggagt gatgacagga acacgggaga     480
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49 aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag      528
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51      1               5                  10                  15

53 cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt      576
54 Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu
55              20                  25                  30

57 tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat      624
58 Trp Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp
59              35                  40                  45

61 tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca      672
62 Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser
63              50                  55                  60

65 cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta      720
66 Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu
67     65                  70                  75

69 tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag      768
70 Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu
71 80                  85                  90                  95

73 gac att agg aaa agc tat cct cac atc att cag gac aaa tgt acc ctt      816
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74  Asp Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu
75              100                 105                 110
77  cac ttt ttg acc cca ggg gtg aat aat tct ggg tca tat att tgt aga      864
78  His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg
79              115                 120                 125
81  ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg      912
82  Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met
83              130                 135                 140
85  att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca      960
86  Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala
87          145                 150                 155
89  tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc     1008
90  Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys
91  160                 165                 170                 175
93  ccc agt ctc agc tgc caa agt gat gca caa agt cca gcg gta acc tgg     1056
94  Pro Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp
95              180                 185                 190
97  tac aag aat gga aaa ctc ctc tct gtg gaa agg agc aac cga atc gta     1104
98  Tyr Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val
99              195                 200                 205
101 gtg gat gaa gtt tat gac tat cac cag ggc aca tat gta tgt gat tac     1152
102 Val Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr
103             210                 215                 220
105 act cag tcg gat act gtg agt tcg tgg aca gtc aga gct gtt gtt caa     1200
106 Thr Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln
107         225                 230                 235
109 gtg aga acc att gtg gga gac act aaa ctc aaa cca gat att ctg gat     1248
110 Val Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp
111 240                 245                 250                 255
113 cct gtc gag gac aca ctg gaa gta gaa ctt gga aag cct tta act att     1296
114 Pro Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile
115             260                 265                 270
117 agc tgc aaa gca cga ttt ggc ttt gaa agg gtc ttt aac cct gtc ata     1344
118 Ser Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile
119         275                 280                 285
121 aaa tgg tac atc aaa gat tct gac cta gag tgg gaa gtc tca gta cct     1392
122 Lys Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro
123         290                 295                 300
125 gag gcg aaa agt att aaa tcc act tta aag gat gaa atc att gag cgt     1440
126 Glu Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg
127 305                 310                 315
129 aat atc atc ttg gaa aaa gtc act cag cgt gat ctt cgc agg aag ttt     1488
130 Asn Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe
131 320                 325                 330                 335
133 gtt tgc ttt gtc cag aac tcc att gga aac aca acc cag tcc gtc caa     1536
134 Val Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln
135             340                 345                 350
137 ctg aaa gaa aag aga gga gtg gtg ctc ctg tac atc ctg ctt ggc acc     1584
138 Leu Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr
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139            355               360               365
141 atc ggg acc ctg gtg gcc gtg ctg gcg gcg agt gcc ctc ctc tac agg    1632
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143            370               375               380
145 cac tgg att gaa ata gtg ctg ctg tac cgg acc tac cag agc aag gat    1680
146 His Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp
147        385               390               395
149 cag acg ctt ggg gat aaa aag gat ttt gat gct ttc gta tcc tat gca    1728
150 Gln Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala
151 400               405               410               415
153 aaa tgg agc tct ttt cca agt gag gcc act tca tct ctg agt gaa gaa    1776
154 Lys Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu
155            420               425               430
157 cac ttg gcc ctg agc cta ttt cct gat gtt tta gaa aac aaa tat gga    1824
158 His Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly
159            435               440               445
161 tat agc ctg tgt ttg ctt gaa aga gat gtg gct cca gga gga gtg tat    1872
162 Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr
163            450               455               460
165 gca gaa gac att gtg agc att att aag aga agc aga aga gga ata ttt    1920
166 Ala Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe
167        465               470               475
169 atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa    1968
170 Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln
171 480               485               490               495
173 gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta    2016
174 Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu
175            500               505               510
177 att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg    2064
178 Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val
179            515               520               525
181 aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa    2112
182 Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys
183            530               535               540
185 tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg    2160
186 Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met
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189 cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc    2208
190 Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr
191 560               565               570               575
193 tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg    2256
194 Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly
195            580               585               590
197 agg agc tcc cag cct aag gaa tgg tga aatgagccct ggagccccct          2303
198 Arg Ser Ser Gln Pro Lys Glu Trp Trp
199            595
201 ccagtccagt ccctgggata gagatgttgc tggacagaac tcacagctct gtgtgtgtgt  2363
203 gttcaggctg ataggaaatt caaagagtct cctgccagca ccaagcaagc ttgatggaca  2423
205 atggaatggg attgagactg tggtttagag cctttgattt cctggactgg acagacggcg  2483
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213 gaaaaaaaac cggaattc                                                  2681
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228             20                  25                  30
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236     50                  55                  60
239 Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser
240 65                  70                  75                  80
243 Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp
244             85                  90                  95
247 Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His
248             100                 105                 110
251 Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro
252         115                 120                 125
255 Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile
256     130                 135                 140
259 Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser
260 145                 150                 155                 160
263 His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro
264             165                 170                 175
267 Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr
268         180                 185                 190
271 Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val
272         195                 200                 205
275 Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr
276     210                 215                 220
279 Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val
280 225                 230                 235                 240
283 Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro
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287 Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser
288             260                 265                 270
291 Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys
292         275                 280                 285
295 Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu
296     290                 295                 300
299 Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn
300 305                 310                 315                 320
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303 Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val
304                 325                 330                 335
307 Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu
308                 340                 345                 350
311 Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile
312         355                 360                 365
315 Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His
316     370                 375                 380
319 Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln
320 385                 390                 395                 400
323 Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys
324                 405                 410                 415
327 Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His
328                 420                 425                 430
331 Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr
332         435                 440                 445
335 Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala
336     450                 455                 460
339 Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile
340 465                 470                 475                 480
343 Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala
344                 485                 490                 495
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348             500                 505                 510
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352         515                 520                 525
355 Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser
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359 Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro
360 545                 550                 555                 560
363 Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser
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378 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY   DATE: 11/02/2001
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number